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Genetics of resistance to *Fusarium udum* in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

Fusarium wilt caused by *Fusarium udum* is an important disease of pigeonpea [*Cajanus cajan* (L.) Millsp.] in Eastern and Southern Africa. Wilted plants often fail to give any yield if attacked early. Several resistant lines have been reported at International Crop Research Institute for Semi-Arid Tropics (ICRISAT). However, this disease has not been well studied genetically. This study was undertaken to determine the mode of inheritance to *Fusarium* wilt in lines which are to be utilised as sources of resistance in the pigeonpea improvement program at the University of Nairobi. Two resistant lines, NPP 725 and NPP 726 were crossed with a susceptible line NPP 718. A cross was also made between the resistant lines. The parents, F_1 and F_2 generations were tested alongside the backcross generations in wilt-sick soil boxes in the glasshouse. Qualitative genetic analyses indicated resistance in both lines to be dominant over susceptibility and controlled by two genes. In the line NPP 725, the gene interaction was inhibitory while in NPP 726, it was complementary. The allelic test between NPP 725 and NPP 726 established independence in these genes. Planned hybridization and backcrossing into local cultivars is already in progress.

Key words: Pigeonpea, *Fusarium* wilt, genetics, complementary, inhibiting, non-allelic

Introduction

All successful breeding programmes designed to produce disease resistant crop varieties start with identifying sources and nature of resistance-conferring genes [1&2]. By knowing whether the resistance being handled is controlled by either one, a few or many genes and also whether it is dominant or recessive to susceptibility, a breeding programme was designed explicitly to meet the target, namely the development of *Fusarium* wilt resistant pigeonpea varieties.

Plant breeding programmes to develop wilt resistant pigeonpea varieties have been underway since the early 1900s, mainly through routine field selection [3&4]. However, little is known about the genetics of this resistance. Information available is limited and largely contradictory. For instance, McRae and Shaw [5] and Green *et al.*, [6] are not categorical on the number of genes involved except to attribute it to "several" genes. Shaw [7] attributed it to either two (9:7) or three (37:27) genes. Joshi [8] thought it is due to a pair of dominant duplicate genes. As to whether it is dominant or not, Shaw [7] found resistance to be dominant over susceptibility. Similar observations were made by Joshi [8] as well. Efforts to link resistance to plant morphological traits for ease of subsequent but indirect selection were not successful [7].

A number of highly resistant lines have been reported by the International Crops Research Institute for the Semi Arid Tropics (ICRISAT) [4]. To date, however, they too have not conclusively determined the number of genes involved in resistance to wilt. Some of their breeders, e.g. K.C. Jain and M.P. Haware (*per. commun.*) only think resistance is recessive to susceptibility and due to several genes. The pigeonpea project of the University of Nairobi obtained some of these lines for its breeding programme. As a starting point, it was decided first to confirm this resistance, then determine its nature and number of genes involved. These findings, it was hoped would assist in formulating a time effective breeding strategy for transferring this resistance into the more adapted cultivars.

Materials and methods

This study was conducted at the University of Nairobi Field Station, Kabete. The genetic materials were developed using three ICRISAT lines, NPP 725 and NPP 726 as the resistant parents and NPP 718 as the susceptible parent. The resistant parents, ICRISAT accessions ICPL 270 and ICP 8863, both early maturing, 165 and 127 days, of short height 139 and 124 cm, respectively, are highly resistant to wilt. However, both have brown small seed (11.6 and 8.5 kg) which is not popular in the Kenyan market. NPP 718 is the ICRISAT accession ICPL 2376. It is very susceptible to wilt. It is also early maturing (135 days), of short height (141 cm) and small seeded (11.3 g) but its color is white.

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Crosses were made between the resistant and susceptible parents and between the resistant parents. The F_1 of each cross was crossed to both parents to raise the backcross populations. All populations - parentals, F_1, F_2, backcross and F_2-derived F_3 line progenies - were screened for wilt resistance using the "sick box" technique. Large wooden boxes (94 × 50 × 34 cm) were used for this test. Each box was filled with wilt-sick soil prepared using the Kimutwa isolate. This is one of the 12 pathotypes of *Fusarium udum* earlier characterised and is very prevalent in the Kenyan pigeonpea growing districts [9]. Other than being widespread, this isolate is also moderately virulent and therefore considered effective in discriminating resistant and susceptible populations. These boxes were laid in two rows in the glasshouse. Eight equidistant furrows were marked in each box and seed of the various generations sown 10 cm apart. About 30 seeds each of the parental, F_1, and backcross populations, between 200-300 of F_2 and several F_2-derived line progenies were used for the study.

Germination counts were made two weeks after planting (WAP) and were used to monitor disease progression. Data on disease expression, i.e. number of plants wilted and non-wilted were recorded at pod maturity. Plants killed by factors other than wilt were discarded and therefore not included in the analysis.

Data obtained were statistically analyzed using the chi-square" test to ascertain the goodness of fit" to different genetic ratios. Since there were only two phenotypic classes, resistant or susceptible, the chi-square formula is modified with Yates' correction factor [10] as shown below:

$$\chi^2 = \sum \frac{[\,|\,(\text{observed} - \text{expected number})\,|\,-0.5)]^2}{\text{expected number}}$$

Results and discussion

Inheritance studies: The results of plant reaction to *Fusarium udum* for all the generations, namely the parents, F_1, F_2, F_3 and backcrosses for all the families are presented in Table 1. As expected, nearly all plants of NPP 725 and NPP 726 were resistant to this isolate while all plants of NPP 718 were susceptible to it.

The F_1 plants from the crosses of NPP 718 with resistant lines NPP 725 and NPP 726 were also resistant just like the resistant parents. The F_2 populations of NPP 725 × NPP 718 cross segregated in a ratio of 13:3 (resistant : susceptible) phenotypic ratio (P>0.05). When backcrossed to resistant parent, NPP 725, the population segregated into a 3 resistant : 1 susceptible phenotypic ratio and to the susceptible it was a 1 : 1 phenotypic ratio. As for the NPP 726 × NPP 718 cross, the F_2 population segregated into 9:7 resistant : susceptible ratio (P>0.05). The backcross (BC_1) population segregated into a phenotypic ratio of 3 resistant : 1 susceptible and to NPP 718 (BC_2) gave all susceptible progeny.

Test for allelism: The F_1 progeny of the NPP 726 × NPP 725 cross and its reciprocal (not shown) were largely resistant to wilt (Table 1). The F_2 and backcross progenies were examined for independence of assortment in the genes of these resistant lines. The F_2 results fitted well into a trigenic segregation ratio of 55 resistant : 9 susceptible (P>0.05). The backcross populations also segregated into ratios comparable to those of F_2 of the respective resistant line.

Fusarium wilt has to date assumed a position of economic importance among pigeonpea growers not only in Kenya but in the entire Eastern and Southern Africa region. This is illustrated by the reports of various scientists [11]. Consequently, all national

Table 1. Resistance to *Fusarium udum*, isolate Kimutwa of lines NPP 725 and NPP 726 and NPP 718, their F_1, F_2 and backcross families

Parents and progeny population	Reaction			Expected ratio	χ^2
	total	resistant	Susceptible		
NPP 725	24	23	1	-	
NPP 726	36	33	3	-	
NPP 718	31	0	31	-	
NPP 725 × NPP 718					
F_1	42	40	2	-	-
F_2	230	181	49	13:3	0.929
BC_1(NPP 725× F_1)	58	43	15	3:1	
BC_2(NPP 725× F_1)	50	28	22	1:1	
F_3 HR	81				
SG	64			7:8:1	
HS	34				
NPP 726 × NPP 718					
F_1	48	48	0	-	-
F_2	260	159	101	9:7	2.669
BC_1(NPP 725× F_1)	36	22	14	3:1	
BC_2(NPP 725× F_1)	24	0	24		
F_3 HR	34				
SG	14			7: 8:1	459.01
HS	62				
NPP 726 × NPP 725					
F_1	55	51	4	-	
F_2	161	141	20	55:9	0.578
BC_1(NPP 725× F_1)	28	22	6		
BC_2(NPP 725× F_1)	36	22	14		
F_3 HR	118				
SG	8			37:26:1	
HS	15				

HR = homozygous resistant; SG = segregating; HS = homozygous susceptible programs have a component on wilt management in their on-going work. Promising and stable resistance is being sought within the countries, region and from outside, especially India. However, the Indian sources, although currently the most reliable, can not be advanced as varieties due to qualities of seed. Thus, they can only be used for breeding. Information on the genetics of resistance in these materials is often lacking and yet it is vital in designing breeding strategies..

The results of this study agree largely with some of the reported findings, namely that resistance is dominant to susceptibility [7, 8] but contradicts the ICRISAT scientists. The dominant nature of this resistance is especially encouraging since its incorporation and selection should be easier than if it were recessive. In NPP 725, the F_2 segregation of 13:3 resistant : susceptible indicated that its resistance is digenic but acting in an inhibitory manner. The segregations in the backcross populations further confirm a two-gene operating system. As for NPP 726, the F_1 as well as the F_2 results showed that its resistance is dominant and also conferred by two genes but these genes were complementary. Its backeross (BC_1) population also segregated into a 3:1 ratio (resistant: susceptible). However, the backcross to the susceptible parent gave all susceptible progeny. This 3:1 ratio, as in the previous population affirms a two-gene condition in NPP 726 as well.

It is important to note, however, that the F_3 populations of both crosses did not segregate in the expected 7:8:1 ($P>0.01$) for homozygous resistant, segregating (resistant/susceptible), and homozygous susceptible respectively. Consequently, the F_3 results were of less assistance in supporting conclusions reached based on F_2 segregating ratios. However, this is not unusual, especially in multigenic resistance where gene interactions exist. Admittedly, even Allard [1] concurs that specifying resistance of the kind reported above is difficult. In fact, the action of modifying genes means that only families homozygous for the two loci are very resistant while variance of resistance will occur. This was the observation here too. Thus, the effect of modifiers and/or complementary genes is the explanation for the observed ratios in the backrosses.

The results of allelic tests not only demonstrated independence in these genes, but also showed that several different genes exist. This is a useful attribute in the development of resistant cultivars of pigeonpea to this fungus that has already been reported to have several pathotypes in the country That there were some segregations in NPP 726 × NPP 725 populations is attributed to modifying genes and either of the complementary genes.

Multigenic resistance is generally accepted as beneficial to work with than monogenic as it is considered more broad and therefore durable. The benefit is even more significant when such resistance is dominant. This is what has been found to exist in these pigeonpea lines. However, it is also true that handling this kind of resistance is cumbersome and difficult. Based on this study, a programme has commenced already to incorporate resistance from NPP 725 and NPP 726 into the local cultivars Munaa, Kioko and NPP 670. It entails crossing and selection using the phenotypic recurrent approach. This is hoped to introduce and increase wilt resistance in the crop. It is expected that response to selection should be rapid given that it is dominant. However, the influence of modifying genes may mar the progress. In conclusion, it can be categorically stated here that the results of this study will be valuable to other breeders in developing adapted, wilt resistant varieties of pigeonpea.

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